



- 1 -

SEQUENCE LISTING

<110> Pawlowski, Krzysztof
Reed, John C.
Godzik, Adam

<120> CARD-DOMAIN CONTAINING POLYPEPTIDES,
ENCODING NUCLEIC ACIDS, AND METHODS OF USE

<130> P-LJ 5100

<140> US 10/032,159

<141> 2001-12-19

<150> US 60/257,457

<151> 2000-12-21

<160> 37

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1101

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1101)

<400> 1

atg	tcg	gac	tac	gag	aac	gat	gac	gag	tgc	tgg	aac	gtc	ctg	gag	ggc	48
Met	Ser	Asp	Tyr	Glu	Asn	Asp	Asp	Glu	Cys	Trp	Asn	Val	Leu	Glu	Gly	
1				5				10					15			

ttc	cgg	gtg	acg	ctc	acc	tcg	gtc	atc	gac	ccc	tca	cgc	atc	aca	cct	96
Phe	Arg	Val	Thr	Leu	Thr	Ser	Val	Ile	Asp	Pro	Ser	Arg	Ile	Thr	Pro	
			20					25					30			

tac	ctg	cgg	cag	tgc	aag	gtc	ctg	aac	cct	gat	gat	gag	gag	cag	gtg	144
Tyr	Leu	Arg	Gln	Cys	Lys	Val	Leu	Asn	Pro	Asp	Asp	Glu	Glu	Gln	Val	
			35				40					45				

ctc	agc	gac	ccc	aac	ctg	gtc	atc	cgc	aaa	cgg	aaa	gtg	ggg	gtg	ctc	192
Leu	Ser	Asp	Pro	Asn	Leu	Val	Ile	Arg	Lys	Arg	Lys	Val	Gly	Val	Leu	
			50				55					60				

ctg	gac	atc	ctg	cag	cgg	acc	ggc	cac	aag	ggc	tac	gtg	gcc	ttc	ctc	240
Leu	Asp	Ile	Leu	Gln	Arg	Thr	Gly	His	Lys	Gly	Tyr	Val	Ala	Phe	Leu	
			65			70				75						80

gag agc ctg gag ctc tac tac ccg' cag ctg tac aag aag gtc aca ggc	288
Glu Ser Leu Glu Leu Tyr Tyr Pro Gln Leu Tyr Lys Lys Val Thr Gly	
85 90 95	
aag gag ccg gcc cgc gtc ttc tcc atg atc atc gac gcg tcc ggg gag	336
Lys Glu Pro Ala Arg Val Phe Ser Met Ile Ile Asp Ala Ser Gly Glu	
100 105 110	
tca ggc ctg act cag ctg ctg atg act gag gtc atg aag ctg cag aag	384
Ser Gly Leu Thr Gln Leu Leu Met Thr Glu Val Met Lys Leu Gln Lys	
115 120 125	
aag gtg cag gac ctg acc gcg ctg ctg agc tcc aaa gat gac ttc atc	432
Lys Val Gln Asp Leu Thr Ala Leu Leu Ser Ser Lys Asp Asp Phe Ile	
130 135 140	
aag gag ctg cgg gtg aag gac agc ctg ctg cgc aag cac cag gag cgt	480
Lys Glu Leu Arg Val Lys Asp Ser Leu Leu Arg Lys His Gln Glu Arg	
145 150 155 160	
gtg cag agg ctc aag gag gag tgc gag gcc gcc agc cgc gag ctc aag	528
Val Gln Arg Leu Lys Glu Glu Cys Glu Ala Gly Ser Arg Glu Leu Lys	
165 170 175	
cgc tgc aag gag gag aac tac gac ctg gcc atg cgc ctg gcg cac cag	576
Arg Cys Lys Glu Glu Asn Tyr Asp Leu Ala Met Arg Leu Ala His Gln	
180 185 190	
agt gag gag aag ggc gcc gcg ctc atg cgg aac cgt gac ctg cag ctg	624
Ser Glu Glu Lys Gly Ala Ala Leu Met Arg Asn Arg Asp Leu Gln Leu	
195 200 205	
gag att gac cag ctc aag cac agc ctc atg aag gcc gag gac gac tgc	672
Glu Ile Asp Gln Leu Lys His Ser Leu Met Lys Ala Glu Asp Asp Cys	
210 215 220	
aag gtg gag cgc aag cac acg ctg aag ctc agg cac gcc atg gag cag	720
Lys Val Glu Arg Lys His Thr Leu Lys Leu Arg His Ala Met Glu Gln	
225 230 235 240	
cgg ccc agc cag gag ctg ctg tgg gag ctg cag cag gag aag gcc ctg	768
Arg Pro Ser Gln Glu Leu Leu Trp Glu Leu Gln Gln Glu Lys Ala Leu	
245 250 255	
ctc cag gcc cgg gtg cag gag ctg gag gcc tcc gtc cag gag ggg aag	816
Leu Gln Ala Arg Val Gln Glu Leu Glu Ala Ser Val Gln Glu Gly Lys	
260 265 270	
ctg gac agg agc agc ccc' tac atc cag gta ctg gag gag gac tgg cgg	864
Leu Asp Arg Ser Ser Pro Tyr Ile Gln Val Leu Glu Glu Asp Trp Arg	
275 280 285	
cag gcg ctg cgg gac cac cag gag cag gcc aac acc atc ttc tcc ctg	912

Gln Ala Leu Arg Asp His Gln Glu Gln Ala Asn Thr Ile Phe Ser Leu
290 295 300

cgc aag gac ctc cgc cag ggc gag gcc cga cgc ctc cgg tgc atg gag 960
Arg Lys Asp Leu Arg Gln Gly Glu Ala Arg Arg Leu Arg Cys Met Glu
305 310 315 320

gag aag gag atg ttc gag ctg cag tgc ctg gca cta cgt aag gac tcc 1008
Glu Lys Glu Met Phe Glu Leu Gln Cys Leu Ala Leu Arg Lys Asp Ser
325 330 335

aag atg tac aag gac cgc atc gag gcc atc ctg ctg cag atg gag gag 1056
Lys Met Tyr Lys Asp Arg Ile Glu Ala Ile Leu Leu Gln Met Glu Glu
340 345 350

gtc gcc att gag cgg gac cag agc aca caa atg gag ggg ctg tga 1101
Val Ala Ile Glu Arg Asp Gln Ser Thr Gln Met Glu Gly Leu *
355 360 365

<210> 2

<211> 366

<212> PRT

<213> Homo sapiens

<400> 2

Met Ser Asp Tyr Glu Asn Asp Asp Glu Cys Trp Asn Val Leu Glu Gly
1 5 10 15
Phe Arg Val Thr Leu Thr Ser Val Ile Asp Pro Ser Arg Ile Thr Pro
20 25 30
Tyr Leu Arg Gln Cys Lys Val Leu Asn Pro Asp Asp Glu Glu Gln Val
35 40 45
Leu Ser Asp Pro Asn Leu Val Ile Arg Lys Arg Lys Val Gly Val Leu
50 55 60
Leu Asp Ile Leu Gln Arg Thr Gly His Lys Gly Tyr Val Ala Phe Leu
65 70 75 80
Glu Ser Leu Glu Leu Tyr Tyr Pro Gln Leu Tyr Lys Lys Val Thr Gly
85 90 95
Lys Glu Pro Ala Arg Val Phe Ser Met Ile Ile Asp Ala Ser Gly Glu
100 105 110
Ser Gly Leu Thr Gln Leu Leu Met Thr Glu Val Met Lys Leu Gln Lys
115 120 125
Lys Val Gln Asp Leu Thr Ala Leu Leu Ser Ser Lys Asp Asp Phe Ile
130 135 140
Lys Glu Leu Arg Val Lys Asp Ser Leu Leu Arg Lys His Gln Glu Arg
145 150 155 160
Val Gln Arg Leu Lys Glu Glu Cys Glu Ala Gly Ser Arg Glu Leu Lys
165 170 175
Arg Cys Lys Glu Glu Asn Tyr Asp Leu Ala Met Arg Leu Ala His Gln
180 185 190
Ser Glu Glu Lys Gly Ala Ala Leu Met Arg Asn Arg Asp Leu Gln Leu
195 200 205

```
<210> 3
<211> 216
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (1) ... (216)
```

<400>	3																	
aac gtc ctg gag ggc ttc cgg gtg acg ctc acc tcg gtc atc gac ccc																	48	
Asn Val Leu Glu Gly Phe Arg Val Thr Leu Thr Ser Val Ile Asp Pro																		
1	5				10							15						
tca cgc atc aca cct tac ctg cgg cag tgc aag gtc ctg aac cct gat																	96	
Ser Arg Ile Thr Pro Tyr Leu Arg Gln Cys Lys Val Leu Asn Pro Asp																		
	20				25							30						
gat gag gag cag gtg ctc agc gac ccc aac ctg gtc atc cgc aaa cgg																	144	
Asp Glu Glu Gln Val Leu Ser Asp Pro Asn Leu Val Ile Arg Lys Arg																		
	35				40							45						
aaa gtg ggt gtg ctc ctg gac atc ctg cag cgg acc ggc cac aag ggc																	192	
Lys Val Gly Val Leu Leu Asp Ile Leu Gln Arg Thr Gly His Lys Gly																		
	50				55							60						
tac gtg gcc ttc ctc gag agc ctg																	216	
Tyr Val Ala Phe Leu Glu Ser Leu																		
65	70																	

<210> 4
 <211> 72
 <212> PRT
 <213> Homo sapiens

<400> 4
 Asn Val Leu Glu Gly Phe Arg Val Thr Leu Thr Ser Val Ile Asp Pro
 1 5 10 15
 Ser Arg Ile Thr Pro Tyr Leu Arg Gln Cys Lys Val Leu Asn Pro Asp
 20 25 30
 Asp Glu Glu Gln Val Leu Ser Asp Pro Asn Leu Val Ile Arg Lys Arg
 35 40 45
 Lys Val Gly Val Leu Leu Asp Ile Leu Gln Arg Thr Gly His Lys Gly
 50 55 60
 Tyr Val Ala Phe Leu Glu Ser Leu
 65 70

<210> 5
 <211> 432
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(432)

<400> 5
 ctg cgc aag cac cag gag cgt gtg cag agg ctc aag gag gag tgc gag 48
 Leu Arg Lys His Gln Glu Arg Val Gln Arg Leu Lys Glu Glu Cys Glu
 1 5 10 15
 gcc ggc agc cgc gag ctc aag cgc tgc aag gag gag aac tac gac ctg 96
 Ala Gly Ser Arg Glu Leu Lys Arg Cys Lys Glu Glu Asn Tyr Asp Leu
 20 25 30
 gcc atg cgc ctg gcg cac cag agt gag gag aag ggc gcc gcg ctc atg 144
 Ala Met Arg Leu Ala His Gln Ser Glu Glu Lys Gly Ala Ala Leu Met
 35 40 45
 cgg aac cgt gac ctg cag ctg gag att gac cag ctc aag cac agc ctc 192
 Arg Asn Arg Asp Leu Gln Leu Glu Ile Asp Gln Leu Lys His Ser Leu
 50 55 60
 atg aag gcc gag gac gac tgc aag gtg gag cgc aag cac acg ctg aag 240
 Met Lys Ala Glu Asp Asp Cys Lys Val Glu Arg Lys His Thr Leu Lys
 65 70 75 80
 ctc agg cac gcc atg gag cag cgg ccc agc cag gag ctg ctg tgg gag 288
 Leu Arg His Ala Met Glu Gln Arg Pro Ser Gln Glu Leu Leu Trp Glu
 85 90 95
 ctg cag cag gag aag gcc ctg ctc cag gcc cgg gtg cag gag ctg gag 336

Leu Gln Gln Glu Lys Ala Leu Leu Gln Ala Arg Val Gln Glu Leu Glu
100 105 110

gcc tcc gtc cag gag ggg aag ctg gac agg agc agc ccc tac atc cag 384
Ala Ser Val Gln Glu Gly Lys Leu Asp Arg Ser Ser Pro Tyr Ile Gln
115 120 125

gta ctg gag gag gac tgg cgg cag gcg ctg cgg gac cac cag gag cag 432
Val Leu Glu Glu Asp Trp Arg Gln Ala Leu Arg Asp His Gln Glu Gln
130 135 140

<210> 6

<211> 144

<212> PRT

<213> Homo sapiens

<400> 6

Leu Arg Lys His Gln Glu Arg Val Gln Arg Leu Lys Glu Glu Cys Glu
1 5 10 15
Ala Gly Ser Arg Glu Leu Lys Arg Cys Lys Glu Glu Asn Tyr Asp Leu
20 25 30
Ala Met Arg Leu Ala His Gln Ser Glu Glu Lys Gly Ala Ala Leu Met
35 40 45
Arg Asn Arg Asp Leu Gln Leu Glu Ile Asp Gln Leu Lys His Ser Leu
50 55 60
Met Lys Ala Glu Asp Asp Cys Lys Val Glu Arg Lys His Thr Leu Lys
65 70 75 80
Leu Arg His Ala Met Glu Gln Arg Pro Ser Gln Glu Leu Leu Trp Glu
85 90 95
Leu Gln Gln Glu Lys Ala Leu Leu Gln Ala Arg Val Gln Glu Leu Glu
100 105 110
Ala Ser Val Gln Glu Gly Lys Leu Asp Arg Ser Ser Pro Tyr Ile Gln
115 120 125
Val Leu Glu Glu Asp Trp Arg Gln Ala Leu Arg Asp His Gln Glu Gln
130 135 140

<210> 7

<211> 3744

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (3744)

<400> 7

atg gat gac tac atg gag acg ctg aag gat gaa gag gac gcc ttg tgg 48
Met Asp Asp Tyr Met Glu Thr Leu Lys Asp Glu Glu Asp Ala Leu Trp
1 5 10 15

gag aat gtg gag tgt aac cgg cac atg ctc agc cgc tat atc aac cct	96
Glu Asn Val Glu Cys Asn Arg His Met Leu Ser Arg Tyr Ile Asn Pro	
20 25 30	
gcc aag ctc acg ccc tac ctg cgt cag tgt aag gtc att gat gag cag	144
Ala Lys Leu Thr Pro Tyr Leu Arg Gln Cys Lys Val Ile Asp Glu Gln	
35 40 45	
gat gaa gat gaa gtg ctt aat gcc cct atg ctg cca tcc aag atc aac	192
Asp Glu Asp Glu Val Leu Asn Ala Pro Met Leu Pro Ser Lys Ile Asn	
50 55 60	
cga gca ggc cgg ctg ttg gac att cta cat acc aag ggg caa agg ggc	240
Arg Ala Gly Arg Leu Leu Asp Ile Leu His Thr Lys Gly Gln Arg Gly	
65 70 75 80	
tat gtg gtc ttc ttg gag agc cta gaa ttt tat tac cca gaa ctg tac	288
Tyr Val Val Phe Leu Glu Ser Leu Glu Phe Tyr Tyr Pro Glu Leu Tyr	
85 90 95	
aaa ctg gtg act ggg aaa gag ccc act cgg aga ttc tcc acc att gtg	336
Lys Leu Val Thr Gly Lys Glu Pro Thr Arg Arg Phe Ser Thr Ile Val	
100 105 110	
gtg gag gaa ggc cac gag ggc ctc acg cac ttc ctg atg aac gag gtc	384
Val Glu Glu Gly His Glu Gly Leu Thr His Phe Leu Met Asn Glu Val	
115 120 125	
atc aag ctg cag cag cag atg aag gcc aag gac ctg caa cgc tgc gag	432
Ile Lys Leu Gln Gln Gln Met Lys Ala Lys Asp Leu Gln Arg Cys Glu	
130 135 140	
ctg ctg gcc agg ttg cgg cag ctg gag gat gag aag aag cag atg acg	480
Leu Leu Ala Arg Leu Arg Gln Leu Glu Asp Glu Lys Lys Gln Met Thr	
145 150 155 160	
ctg acg cgc gtg gag ctg cta acc ttc cag gag cgg tac tac aag atg	528
Leu Thr Arg Val Glu Leu Leu Thr Phe Gln Glu Arg Tyr Tyr Lys Met	
165 170 175	
aag gaa gag cgg gac agc tac aat gac gag ctg gtc aag gtg aag gac	576
Lys Glu Glu Arg Asp Ser Tyr Asn Asp Glu Leu Val Lys Val Lys Asp	
180 185 190	
gac aac tac aac tta gcc atg cgc tac gca cag ctc agt gag gag aag	624
Asp Asn Tyr Asn Leu Ala Met Arg Tyr Ala Gln Leu Ser Glu Glu Lys	
195 200 205	
aac atg gcg gtc atg agg agc cga gac ctc caa ctc gag atc gat cag	672
Asn Met Ala Val Met Arg Ser Arg Asp Leu Gln Leu Glu Ile Asp Gln	
210 215 220	
cta aag cac cgg ttg aat aag atg gag gag gaa tgt aag ctg gag aga	720

Leu Lys His Arg	Leu Asn Lys Met	Glu Glu Glu Cys Lys	Leu Glu Arg	
225	230	235	240	
aat cag tct cta	aaa ctg aag aat gac	att gaa aat cgg	ccc aag aag	768
Asn Gln Ser Leu	Lys Leu Lys Asn Asp	Ile Glu Asn Arg	Pro Lys Lys	
	245	250	255	
gag cag gtt ctg	gaa ctg gag cgg	gag aat gaa atg	ctg aag acc aaa	816
Glu Gln Val Leu	Glu Leu Glu Arg	Glu Asn Glu Met	Leu Lys Thr Lys	
	260	265	270	
aac cag gag ctg	cag tcc atc atc	cag gcc ggg aag	cgc agc ctg cca	864
Asn Gln Glu Leu	Gln Ser Ile Ile	Gln Ala Gly Lys	Arg Ser Leu Pro	
	275	280	285	
gac tca gac aag	gcc atc ctg gac	atc ttg gaa cac	gac cgc aag gag	912
Asp Ser Asp Lys	Ala Ile Leu Asp	Ile Leu Glu His	Asp Arg Lys Glu	
	290	295	300	
gcc ctg gag gac	agg cag gag ctg	gtc aac agg atc	tac aac ctg cag	960
Ala Leu Glu Asp	Arg Gln Glu Leu	Val Asn Arg Ile	Tyr Asn Leu Gln	
	305	310	315	320
gag gag gcc cgc	cag gca gag gag	ctg cga gac aag	tac ctg gag gag	1008
Glu Glu Ala Arg	Gln Ala Glu Glu	Leu Arg Asp Lys	Tyr Leu Glu Glu	
	325	330	335	
aag gag gac ctg	gag ctc aag tgc	tcg acc ctg gga	aag gac tgt gaa	1056
Lys Glu Asp Leu	Glu Leu Lys Cys	Ser Thr Leu Gly	Lys Asp Cys Glu	
	340	345	350	
atg tac aag cac	cgc atg aac acg	gtc atg ctg cag	ctg gag gag gtg	1104
Met Tyr Lys His	Arg Met Asn Thr	Val Met Leu Gln	Leu Glu Glu Val	
	355	360	365	
gag cgg gag cgg	gac cag gga cag	gct gtg gcc ttc	cag gga cac tgc	1152
Glu Arg Glu Arg	Asp Gln Gly Gln	Ala Val Ala Phe	Gln Gly His Cys	
	370	375	380	
atc aaa gct ctc	aac aca gag cct	gcc act agc aag	ggt cgg acc atc	1200
Ile Lys Ala Leu	Asn Thr Glu Pro	Ala Thr Ser Lys	Gly Arg Thr Ile	
	385	390	395	400
ggc tct gtg atc	gcg tta atg aag	aag gcc ttc cac	tcc cga gat gaa	1248
Gly Ser Val Ile	Ala Leu Met Lys	Lys Ala Phe His	Ser Arg Asp Glu	
	405	410	415	
gct cag aca cag	tac tcg cag tgc	tta atc gaa aag	gac aag tac agg	1296
Ala Gln Thr Gln	Tyr Ser Gln Cys	Leu Ile Glu Lys	Asp Lys Tyr Arg	
	420	425	430	
aag cag atc cgc	gag ctg gag gag	aag aac gac gag	atg agg atc gag	1344
Lys Gln Ile Arg	Glu Leu Glu Glu	Lys Asn Asp Glu	Met Arg Ile Glu	

435	440	445	
atg gtg cgg cgg gag gcc tgc atc gtc aac ctg gag agc aag ctg cgg			1392
Met Val Arg Arg Glu Ala Cys Ile Val Asn Leu Glu Ser Lys Leu Arg			
450	455	460	
cgc ctc tcc aag gac agc aac aac ctg gac cag agt ctg ccc agg aac			1440
Arg Leu Ser Lys Asp Ser Asn Asn Leu Asp Gln Ser Leu Pro Arg Asn			
465	470	475	480
ctg cca gta acc atc atc tct cag gac ttt ggg gat gcc agc ccc agg			1488
Leu Pro Val Thr Ile Ile Ser Gln Asp Phe Gly Asp Ala Ser Pro Arg			
485	490	495	
acc aat ggt caa gaa gct gac gat tct tcc acc tcg gag gag tca cct			1536
Thr Asn Gly Gln Glu Ala Asp Asp Ser Ser Thr Ser Glu Glu Ser Pro			
500	505	510	
gaa gac agc aag tac ttc ctg ccc tac cat ccg ccc cag cgc agg atg			1584
Glu Asp Ser Lys Tyr Phe Leu Pro Tyr His Pro Pro Gln Arg Arg Met			
515	520	525	
aac ctg aag ggc atc cag ctg cag aga gcc aaa tcc ccc atc agc ctg			1632
Asn Leu Lys Gly Ile Gln Leu Gln Arg Ala Lys Ser Pro Ile Ser Leu			
530	535	540	
aag cga aca tca gat ttt caa gcc aag ggg cac gag gaa gaa ggc acg			1680
Lys Arg Thr Ser Asp Phe Gln Ala Lys Gly His Glu Glu Glu Gly Thr			
545	550	555	560
gac gcc agc cct agc tcc tgc gga tct ctg ccc atc acc aac tcc ttc			1728
Asp Ala Ser Pro Ser Ser Cys Gly Ser Leu Pro Ile Thr Asn Ser Phe			
565	570	575	
acc aag atg ccc ccc cgg agc cgc agc agc atc atg tca atc acc gcc			1776
Thr Lys Met Pro Pro Arg Ser Arg Ser Ser Ile Met Ser Ile Thr Ala			
580	585	590	
gag ccc ccg gga aac gac tcc atc gtc aga cgc tac aag gag gac gcg			1824
Glu Pro Pro Gly Asn Asp Ser Ile Val Arg Arg Tyr Lys Glu Asp Ala			
595	600	605	
ccc cat cgc agc aca gtc gaa gaa gac aat gac agc ggc ggg ttt gac			1872
Pro His Arg Ser Thr Val Glu Glu Asp Asn Asp Ser Gly Gly Phe Asp			
610	615	620	
gcc tta gat ctg gat gag ctg gca gca ggg gag act gtg gct cag agt			1920
Ala Leu Asp Leu Asp Glu Leu Ala Ala Gly Glu Thr Val Ala Gln Ser			
625	630	635	640
cct cca ggt gtg ccc tgc cag ccc cct ctc ttc cag ggc tcc ccc agc			1968
Pro Pro Gly Val Pro Cys Gln Pro Pro Leu Phe Gln Gly Ser Pro Ser			
645	650	655	

ctt tgc cag cta agg ctg cca acc gat gaa acg aaa gat gag tgg tcc	2016
Leu Cys Gln Leu Arg Leu Pro Thr Asp Glu Thr Lys Asp Glu Trp Ser	
660 665 670	
tcc tta atg ggg aag cat cag cgc tac caa gtg tta aag aga gat gac	2064
Ser Leu Met Gly Lys His Gln Arg Tyr Gln Val Leu Lys Arg Asp Asp	
675 680 685	
agt cac gaa cgc tac tcc ttc gga ccc tcc tcc atc cac tcc tcc tcc	2112
Ser His Glu Arg Tyr Ser Phe Gly Pro Ser Ser Ile His Ser Ser Ser	
690 695 700	
tcc tcc cac caa tcc gag ggc ctg gat gcc tac gac ctg gag cag gtc	2160
Ser Ser His Gln Ser Glu Gly Leu Asp Ala Tyr Asp Leu Glu Gln Val	
705 710 715 720	
aac ctc atg ttc agg aag ttc tct ctg gaa aga ccc ttc cgg cct tcg	2208
Asn Leu Met Phe Arg Lys Phe Ser Leu Glu Arg Pro Phe Arg Pro Ser	
725 730 735	
gtc acc tct gtg ggg cac gtg cgg ggc cca ggg ccc tcg gtg cag cac	2256
Val Thr Ser Val Gly His Val Arg Gly Pro Gly Pro Ser Val Gln His	
740 745 750	
acg acg ctg aat ggc gac agc ctc acc tcc cag ctc acc ctg ctg ggg	2304
Thr Thr Leu Asn Gly Asp Ser Leu Thr Ser Gln Leu Thr Leu Leu Gly	
755 760 765	
ggc aac gcg cga ggg agc ttc gtg cac tcg gtc aag cct ggc tct ctg	2352
Gly Asn Ala Arg Gly Ser Phe Val His Ser Val Lys Pro Gly Ser Leu	
770 775 780	
gcc gag aaa gcc ggc ctc cgt gag ggc cac cag ctg ctg ctg cta gaa	2400
Ala Glu Lys Ala Gly Leu Arg Glu Gly His Gln Leu Leu Leu Leu Glu	
785 790 795 800	
ggc tgc atc cga ggc gag agg cag agt gtc ccg ttg gac aca tgc acc	2448
Gly Cys Ile Arg Gly Glu Arg Gln Ser Val Pro Leu Asp Thr Cys Thr	
805 810 815	
aaa gag gaa gcc cac tgg acc atc cag agg tgc agc ggc ccc gtc acg	2496
Lys Glu Glu Ala His Trp Thr Ile Gln Arg Cys Ser Gly Pro Val Thr	
820 825 830	
ctg cac tac aag gtc aac cac gaa gcc cag cag aaa atc cgt ggg cct	2544
Leu His Tyr Lys Val Asn His Glu Ala Gln Gln Lys Ile Arg Gly Pro	
835 840 845	
gca gaa tat gat gtg ggc agc acc tcc aaa gcc cgg agc tgc gca gca	2592
Ala Glu Tyr Asp Val Gly Ser Thr Ser Lys Ala Arg Ser Cys Ala Ala	
850 855 860	

gca cag ccc tgc aag tct gga att' cca ggg aaa gaa agt tca ttc cgg	2640
Ala Gln Pro Cys Lys Ser Gly Ile Pro Gly Lys Glu Ser Ser Phe Arg	
865 870 875 880	
cag ggg tac cgg aag ctg gtg aag gac atg gag gac ggc ctg atc aca	2688
Gln Gly Tyr Arg Lys Leu Val Lys Asp Met Glu Asp Gly Leu Ile Thr	
885 890 895	
tcg ggg gac tcg ttc tac atc cgg ctg aac ctg aac atc tcc agc cag	2736
Ser Gly Asp Ser Phe Tyr Ile Arg Leu Asn Leu Asn Ile Ser Ser Gln	
900 905 910	
ctg gac gcc tgc acc atg tcc ctg aag tgt gac gat gtt gtg cac gtc	2784
Leu Asp Ala Cys Thr Met Ser Leu Lys Cys Asp Asp Val Val His Val	
915 920 925	
cgt gac acc atg tac cag gac agg cac gag tgg ctg tgc gcg cgg gtc	2832
Arg Asp Thr Met Tyr Gln Asp Arg His Glu Trp Leu Cys Ala Arg Val	
930 935 940	
gac cct ttc aca gac cat gac ctg gat atg ggc acc ata ccc agc tac	2880
Asp Pro Phe Thr Asp His Asp Leu Asp Met Gly Thr Ile Pro Ser Tyr	
945 950 955 960	
agc cga gcc cag cag ctc ctc ctg gtg aaa ctg cag cgc ctg atg cac	2928
Ser Arg Ala Gln Gln Leu Leu Val Lys Leu Gln Arg Leu Met His	
965 970 975	
cga ggc agc cgg gag gag gta gac ggc acc cac cac acc ctg cgg gca	2976
Arg Gly Ser Arg Glu Glu Val Asp Gly Thr His His Thr Leu Arg Ala	
980 985 990	
ctc cgg ttc gtc agc agg tcc gag aac aag tat aag cgg atg aac agc	3024
Leu Arg Phe Val Ser Arg Ser Glu Asn Lys Tyr Lys Arg Met Asn Ser	
995 1000 1005	
aat gag cgg gtc cgc atc atc tcg ggg agt ccg cta ggg agc ctg gcc	3072
Asn Glu Arg Val Arg Ile Ile Ser Gly Ser Pro Leu Gly Ser Leu Ala	
1010 1015 1020	
cgg tcc tcg ctg gac gcc acc aag ctc ttg act gag aag cag gaa gag	3120
Arg Ser Ser Leu Asp Ala Thr Lys Leu Leu Thr Glu Lys Gln Glu Glu	
1025 1030 1035 1040	
ctg gac cct gag agc gag ctg ggc aag aac ctc agc ctc atc ccc tac	3168
Leu Asp Pro Glu Ser Glu Leu Gly Lys Asn Leu Ser Leu Ile Pro Tyr	
1045 1050 1055	
agc ctg gta cgc gcc ttc tac tgc gag cgc cgc cgg ccc gtg ctc ttc	3216
Ser Leu Val Arg Ala Phe Tyr Cys Glu Arg Arg Arg Pro Val Leu Phe	
1060 1065 1070	
aca ccc acc gtg ctg gcc aag acg ctg gtg cag agg ctg ctc aac tcg	3264

Thr	Pro	Thr	Val	Leu	Ala	Lys	Thr	Leu	Val	Gln	Arg	Leu	Leu	Asn	Ser		
				1075					1080					1085			
gga	ggt	gcc	atg	gag	ttc	acc	atc	tgc	aag	tca	gat	atc	gtc	aca	aga	3312	
Gly	Gly	Ala	Met	Glu	Phe	Thr	Ile	Cys	Lys	Ser	Asp	Ile	Val	Thr	Arg		
		1090					1095					1100					
gat	gag	ttc	ctc	aga	agg	cag	aag	acg	gag	acc	atc	atc	tac	tcc	cga	3360	
Asp	Glu	Phe	Leu	Arg	Arg	Gln	Lys	Thr	Glu	Thr	Ile	Ile	Tyr	Ser	Arg		
1105					1110					1115					1120		
gag	aag	aac	ccc	aac	gcg	ttc	gaa	tgc	atc	gcc	cct	gcc	aac	att	gaa	3408	
Glu	Lys	Asn	Pro	Asn	Ala	Phe	Glu	Cys	Ile	Ala	Pro	Ala	Asn	Ile	Glu		
				1125					1130					1135			
gct	gtg	gcc	gcc	aag	aac	aag	cac	tgc	ctg	ctg	gag	gct	ggg	atc	ggc	3456	
Ala	Val	Ala	Ala	Lys	Asn	Lys	His	Cys	Leu	Leu	Glu	Ala	Gly	Ile	Gly		
			1140					1145					1150				
tgc	aca	aga	gac	ttg	atc	aag	tcc	aac	atc	tac	ccc	atc	gtg	ctc	ttc	3504	
Cys	Thr	Arg	Asp	Leu	Ile	Lys	Ser	Asn	Ile	Tyr	Pro	Ile	Val	Leu	Phe		
		1155					1160					1165					
atc	cgg	gtg	tgt	gag	aag	aac	atc	aag	agg	ttc	aga	aag	ctg	ctg	ccc	3552	
Ile	Arg	Val	Cys	Glu	Lys	Asn	Ile	Lys	Arg	Phe	Arg	Lys	Leu	Leu	Pro		
	1170					1175					1180						
cgg	cct	gag	acg	gag	gag	gag	ttc	ctg	cgc	gtg	tgc	cgg	ctg	aag	gag	3600	
Arg	Pro	Glu	Thr	Glu	Glu	Glu	Phe	Leu	Arg	Val	Cys	Arg	Leu	Lys	Glu		
1185					1190					1195					1200		
aag	gag	ctg	gag	gcc	ctg	ccg	tgc	ctg	tac	gcc	acg	gtg	gaa	cct	gac	3648	
Lys	Glu	Leu	Glu	Ala	Leu	Pro	Cys	Leu	Tyr	Ala	Thr	Val	Glu	Pro	Asp		
				1205					1210					1215			
atg	tgg	ggc	agc	gta	gag	gag	ctg	ctc	cgc	gtt	gtc	aag	gac	aag	atc	3696	
Met	Trp	Gly	Ser	Val	Glu	Glu	Leu	Leu	Arg	Val	Val	Lys	Asp	Lys	Ile		
		1220						1225					1230				
ggc	gag	gag	cag	cgc	aag	acc	atc	tgg	gtg	gac	gag	gac	cag	ctg	tga	3744	
Gly	Glu	Glu	Gln	Arg	Lys	Thr	Ile	Trp	Val	Asp	Glu	Asp	Gln	Leu	*		
		1235					1240					1245					

<210> 8

<211> 1247

<212> PRT

<213> Homo sapiens

<400> 8

Met	Asp	Asp	Tyr	Met	Glu	Thr	Leu	Lys	Asp	Glu	Glu	Asp	Ala	Leu	Trp
1				5				10						15	

Glu	Asn	Val	Glu	Cys	Asn	Arg	His	Met	Leu	Ser	Arg	Tyr	Ile	Asn	Pro
		20						25					30		
Ala	Lys	Leu	Thr	Pro	Tyr	Leu	Arg	Gln	Cys	Lys	Val	Ile	Asp	Glu	Gln
		35					40					45			
Asp	Glu	Asp	Glu	Val	Leu	Asn	Ala	Pro	Met	Leu	Pro	Ser	Lys	Ile	Asn
	50					55					60				
Arg	Ala	Gly	Arg	Leu	Leu	Asp	Ile	Leu	His	Thr	Lys	Gly	Gln	Arg	Gly
65					70					75					80
Tyr	Val	Val	Phe	Leu	Glu	Ser	Leu	Glu	Phe	Tyr	Tyr	Pro	Glu	Leu	Tyr
			85						90					95	
Lys	Leu	Val	Thr	Gly	Lys	Glu	Pro	Thr	Arg	Arg	Phe	Ser	Thr	Ile	Val
			100					105					110		
Val	Glu	Glu	Gly	His	Glu	Gly	Leu	Thr	His	Phe	Leu	Met	Asn	Glu	Val
		115					120					125			
Ile	Lys	Leu	Gln	Gln	Gln	Met	Lys	Ala	Lys	Asp	Leu	Gln	Arg	Cys	Glu
	130					135					140				
Leu	Leu	Ala	Arg	Leu	Arg	Gln	Leu	Glu	Asp	Glu	Lys	Lys	Gln	Met	Thr
145					150					155					160
Leu	Thr	Arg	Val	Glu	Leu	Leu	Thr	Phe	Gln	Glu	Arg	Tyr	Tyr	Lys	Met
			165						170					175	
Lys	Glu	Glu	Arg	Asp	Ser	Tyr	Asn	Asp	Glu	Leu	Val	Lys	Val	Lys	Asp
			180					185					190		
Asp	Asn	Tyr	Asn	Leu	Ala	Met	Arg	Tyr	Ala	Gln	Leu	Ser	Glu	Glu	Lys
	195						200					205			
Asn	Met	Ala	Val	Met	Arg	Ser	Arg	Asp	Leu	Gln	Leu	Glu	Ile	Asp	Gln
	210					215					220				
Leu	Lys	His	Arg	Leu	Asn	Lys	Met	Glu	Glu	Glu	Cys	Lys	Leu	Glu	Arg
225					230					235					240
Asn	Gln	Ser	Leu	Lys	Leu	Lys	Asn	Asp	Ile	Glu	Asn	Arg	Pro	Lys	Lys
			245						250					255	
Glu	Gln	Val	Leu	Glu	Leu	Glu	Arg	Glu	Asn	Glu	Met	Leu	Lys	Thr	Lys
		260						265					270		
Asn	Gln	Glu	Leu	Gln	Ser	Ile	Ile	Gln	Ala	Gly	Lys	Arg	Ser	Leu	Pro
		275					280					285			
Asp	Ser	Asp	Lys	Ala	Ile	Leu	Asp	Ile	Leu	Glu	His	Asp	Arg	Lys	Glu
	290					295					300				
Ala	Leu	Glu	Asp	Arg	Gln	Glu	Leu	Val	Asn	Arg	Ile	Tyr	Asn	Leu	Gln
305					310					315					320
Glu	Glu	Ala	Arg	Gln	Ala	Glu	Glu	Leu	Arg	Asp	Lys	Tyr	Leu	Glu	Glu
			325						330					335	
Lys	Glu	Asp	Leu	Glu	Leu	Lys	Cys	Ser	Thr	Leu	Gly	Lys	Asp	Cys	Glu
		340						345					350		
Met	Tyr	Lys	His	Arg	Met	Asn	Thr	Val	Met	Leu	Gln	Leu	Glu	Glu	Val
	355						360					365			
Glu	Arg	Glu	Arg	Asp	Gln	Gly	Gln	Ala	Val	Ala	Phe	Gln	Gly	His	Cys
	370					375					380				
Ile	Lys	Ala	Leu	Asn	Thr	Glu	Pro	Ala	Thr	Ser	Lys	Gly	Arg	Thr	Ile
385					390					395					400
Gly	Ser	Val	Ile	Ala	Leu	Met	Lys	Lys	Ala	Phe	His	Ser	Arg	Asp	Glu
			405						410					415	
Ala	Gln	Thr	Gln	Tyr	Ser	Gln	Cys	Leu	Ile	Glu	Lys	Asp	Lys	Tyr	Arg
		420						425				430			
Lys	Gln	Ile	Arg	Glu	Leu	Glu	Glu	Lys	Asn	Asp	Glu	Met	Arg	Ile	Glu

435					440					445					
Met	Val	Arg	Arg	Glu	Ala	Cys	Ile	Val	Asn	Leu	Glu	Ser	Lys	Leu	Arg
450					455					460					
Arg	Leu	Ser	Lys	Asp	Ser	Asn	Asn	Leu	Asp	Gln	Ser	Leu	Pro	Arg	Asn
465					470					475					480
Leu	Pro	Val	Thr	Ile	Ile	Ser	Gln	Asp	Phe	Gly	Asp	Ala	Ser	Pro	Arg
					485					490					495
Thr	Asn	Gly	Gln	Glu	Ala	Asp	Asp	Ser	Ser	Thr	Ser	Glu	Glu	Ser	Pro
					500					505					510
Glu	Asp	Ser	Lys	Tyr	Phe	Leu	Pro	Tyr	His	Pro	Pro	Gln	Arg	Arg	Met
					515					520					525
Asn	Leu	Lys	Gly	Ile	Gln	Leu	Gln	Arg	Ala	Lys	Ser	Pro	Ile	Ser	Leu
					530					535					540
Lys	Arg	Thr	Ser	Asp	Phe	Gln	Ala	Lys	Gly	His	Glu	Glu	Glu	Gly	Thr
545					550					555					560
Asp	Ala	Ser	Pro	Ser	Ser	Cys	Gly	Ser	Leu	Pro	Ile	Thr	Asn	Ser	Phe
					565					570					575
Thr	Lys	Met	Pro	Pro	Arg	Ser	Arg	Ser	Ser	Ile	Met	Ser	Ile	Thr	Ala
					580					585					590
Glu	Pro	Pro	Gly	Asn	Asp	Ser	Ile	Val	Arg	Arg	Tyr	Lys	Glu	Asp	Ala
					595					600					605
Pro	His	Arg	Ser	Thr	Val	Glu	Glu	Asp	Asn	Asp	Ser	Gly	Gly	Phe	Asp
					610					615					620
Ala	Leu	Asp	Leu	Asp	Glu	Leu	Ala	Ala	Gly	Glu	Thr	Val	Ala	Gln	Ser
625					630					635					640
Pro	Pro	Gly	Val	Pro	Cys	Gln	Pro	Pro	Leu	Phe	Gln	Gly	Ser	Pro	Ser
					645					650					655
Leu	Cys	Gln	Leu	Arg	Leu	Pro	Thr	Asp	Glu	Thr	Lys	Asp	Glu	Trp	Ser
					660					665					670
Ser	Leu	Met	Gly	Lys	His	Gln	Arg	Tyr	Gln	Val	Leu	Lys	Arg	Asp	Asp
					675					680					685
Ser	His	Glu	Arg	Tyr	Ser	Phe	Gly	Pro	Ser	Ser	Ile	His	Ser	Ser	Ser
					690					695					700
Ser	Ser	His	Gln	Ser	Glu	Gly	Leu	Asp	Ala	Tyr	Asp	Leu	Glu	Gln	Val
705					710					715					720
Asn	Leu	Met	Phe	Arg	Lys	Phe	Ser	Leu	Glu	Arg	Pro	Phe	Arg	Pro	Ser
					725					730					735
Val	Thr	Ser	Val	Gly	His	Val	Arg	Gly	Pro	Gly	Pro	Ser	Val	Gln	His
					740					745					750
Thr	Thr	Leu	Asn	Gly	Asp	Ser	Leu	Thr	Ser	Gln	Leu	Thr	Leu	Leu	Gly
					755					760					765
Gly	Asn	Ala	Arg	Gly	Ser	Phe	Val	His	Ser	Val	Lys	Pro	Gly	Ser	Leu
					770					775					780
Ala	Glu	Lys	Ala	Gly	Leu	Arg	Glu	Gly	His	Gln	Leu	Leu	Leu	Leu	Glu
785					790					795					800
Gly	Cys	Ile	Arg	Gly	Glu	Arg	Gln	Ser	Val	Pro	Leu	Asp	Thr	Cys	Thr
					805					810					815
Lys	Glu	Glu	Ala	His	Trp	Thr	Ile	Gln	Arg	Cys	Ser	Gly	Pro	Val	Thr
					820					825					830
Leu	His	Tyr	Lys	Val	Asn	His	Glu	Ala	Gln	Gln	Lys	Ile	Arg	Gly	Pro
					835					840					845
Ala	Glu	Tyr	Asp	Val	Gly	Ser	Thr	Ser	Lys	Ala	Arg	Ser	Cys	Ala	Ala
					850					855					860

Ala	Gln	Pro	Cys	Lys	Ser	Gly	Ile	Pro	Gly	Lys	Glu	Ser	Ser	Phe	Arg
865					870					875					880
Gln	Gly	Tyr	Arg	Lys	Leu	Val	Lys	Asp	Met	Glu	Asp	Gly	Leu	Ile	Thr
				885					890						895
Ser	Gly	Asp	Ser	Phe	Tyr	Ile	Arg	Leu	Asn	Leu	Asn	Ile	Ser	Ser	Gln
			900					905					910		
Leu	Asp	Ala	Cys	Thr	Met	Ser	Leu	Lys	Cys	Asp	Asp	Val	Val	His	Val
		915					920					925			
Arg	Asp	Thr	Met	Tyr	Gln	Asp	Arg	His	Glu	Trp	Leu	Cys	Ala	Arg	Val
	930					935					940				
Asp	Pro	Phe	Thr	Asp	His	Asp	Leu	Asp	Met	Gly	Thr	Ile	Pro	Ser	Tyr
945					950					955					960
Ser	Arg	Ala	Gln	Gln	Leu	Leu	Leu	Val	Lys	Leu	Gln	Arg	Leu	Met	His
			965						970						975
Arg	Gly	Ser	Arg	Glu	Glu	Val	Asp	Gly	Thr	His	His	Thr	Leu	Arg	Ala
			980					985					990		
Leu	Arg	Phe	Val	Ser	Arg	Ser	Glu	Asn	Lys	Tyr	Lys	Arg	Met	Asn	Ser
		995					1000					1005			
Asn	Glu	Arg	Val	Arg	Ile	Ile	Ser	Gly	Ser	Pro	Leu	Gly	Ser	Leu	Ala
	1010					1015					1020				
Arg	Ser	Ser	Leu	Asp	Ala	Thr	Lys	Leu	Leu	Thr	Glu	Lys	Gln	Glu	Glu
1025				1030						1035					1040
Leu	Asp	Pro	Glu	Ser	Glu	Leu	Gly	Lys	Asn	Leu	Ser	Leu	Ile	Pro	Tyr
			1045					1050						1055	
Ser	Leu	Val	Arg	Ala	Phe	Tyr	Cys	Glu	Arg	Arg	Arg	Pro	Val	Leu	Phe
		1060						1065					1070		
Thr	Pro	Thr	Val	Leu	Ala	Lys	Thr	Leu	Val	Gln	Arg	Leu	Leu	Asn	Ser
		1075					1080					1085			
Gly	Gly	Ala	Met	Glu	Phe	Thr	Ile	Cys	Lys	Ser	Asp	Ile	Val	Thr	Arg
	1090					1095					1100				
Asp	Glu	Phe	Leu	Arg	Arg	Gln	Lys	Thr	Glu	Thr	Ile	Ile	Tyr	Ser	Arg
1105					1110					1115					1120
Glu	Lys	Asn	Pro	Asn	Ala	Phe	Glu	Cys	Ile	Ala	Pro	Ala	Asn	Ile	Glu
			1125					1130						1135	
Ala	Val	Ala	Ala	Lys	Asn	Lys	His	Cys	Leu	Leu	Glu	Ala	Gly	Ile	Gly
			1140					1145					1150		
Cys	Thr	Arg	Asp	Leu	Ile	Lys	Ser	Asn	Ile	Tyr	Pro	Ile	Val	Leu	Phe
		1155					1160					1165			
Ile	Arg	Val	Cys	Glu	Lys	Asn	Ile	Lys	Arg	Phe	Arg	Lys	Leu	Leu	Pro
	1170					1175					1180				
Arg	Pro	Glu	Thr	Glu	Glu	Glu	Phe	Leu	Arg	Val	Cys	Arg	Leu	Lys	Glu
1185					1190					1195					1200
Lys	Glu	Leu	Glu	Ala	Leu	Pro	Cys	Leu	Tyr	Ala	Thr	Val	Glu	Pro	Asp
			1205					1210					1215		
Met	Trp	Gly	Ser	Val	Glu	Glu	Leu	Leu	Arg	Val	Val	Lys	Asp	Lys	Ile
			1220					1225				1230			
Gly	Glu	Glu	Gln	Arg	Lys	Thr	Ile	Trp	Val	Asp	Glu	Asp	Gln	Leu	
	1235						1240					1245			

<210> 9

<211> 276

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(276)

<400> 9

gag	gac	gcc	ttg	tgg	gag	aat	gtg	gag	tgt	aac	cgg	cac	atg	ctc	agc	48
Glu	Asp	Ala	Leu	Trp	Glu	Asn	Val	Glu	Cys	Asn	Arg	His	Met	Leu	Ser	
1			5					10					15			

cgc	tat	atc	aac	cct	gcc	aag	ctc	acg	ccc	tac	ctg	cgt	cag	tgt	aag	96
Arg	Tyr	Ile	Asn	Pro	Ala	Lys	Leu	Thr	Pro	Tyr	Leu	Arg	Gln	Cys	Lys	
		20					25					30				

gtc	att	gat	gag	cag	gat	gaa	gat	gaa	gtg	ctt	aat	gcc	cct	atg	ctg	144
Val	Ile	Asp	Glu	Gln	Asp	Glu	Asp	Glu	Val	Leu	Asn	Ala	Pro	Met	Leu	
		35				40					45					

cca	tcc	aag	atc	aac	cga	gca	ggc	cgg	ctg	ttg	gac	att	cta	cat	acc	192
Pro	Ser	Lys	Ile	Asn	Arg	Ala	Gly	Arg	Leu	Leu	Asp	Ile	Leu	His	Thr	
		50				55					60					

aag	ggg	caa	agg	ggc	tat	gtg	gtc	ttc	ttg	gag	agc	cta	gaa	ttt	tat	240
Lys	Gly	Gln	Arg	Gly	Tyr	Val	Val	Phe	Leu	Glu	Ser	Leu	Glu	Phe	Tyr	
65					70				75						80	

tac	cca	gaa	ctg	tac	aaa	ctg	gtg	act	ggg	aaa	gag					276
Tyr	Pro	Glu	Leu	Tyr	Lys	Leu	Val	Thr	Gly	Lys	Glu					
			85					90								

<210> 10

<211> 92

<212> PRT

<213> Homo sapiens

<400> 10

Glu	Asp	Ala	Leu	Trp	Glu	Asn	Val	Glu	Cys	Asn	Arg	His	Met	Leu	Ser	
1			5					10					15			
Arg	Tyr	Ile	Asn	Pro	Ala	Lys	Leu	Thr	Pro	Tyr	Leu	Arg	Gln	Cys	Lys	
		20					25					30				
Val	Ile	Asp	Glu	Gln	Asp	Glu	Asp	Glu	Val	Leu	Asn	Ala	Pro	Met	Leu	
		35				40					45					
Pro	Ser	Lys	Ile	Asn	Arg	Ala	Gly	Arg	Leu	Leu	Asp	Ile	Leu	His	Thr	
		50				55					60					
Lys	Gly	Gln	Arg	Gly	Tyr	Val	Val	Phe	Leu	Glu	Ser	Leu	Glu	Phe	Tyr	
65					70				75						80	
Tyr	Pro	Glu	Leu	Tyr	Lys	Leu	Val	Thr	Gly	Lys	Glu					
			85					90								

<210> 11

<211> 957
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(957)

<400> 11
aag ctg cag cag cag atg aag gcc aag gac ctg caa cgc tgc gag ctg 48
Lys Leu Gln Gln Gln Met Lys Ala Lys Asp Leu Gln Arg Cys Glu Leu
1 5 10 15
ctg gcc agg ttg cgg cag ctg gag gat gag aag aag cag atg acg ctg 96
Leu Ala Arg Leu Arg Gln Leu Glu Asp Glu Lys Lys Gln Met Thr Leu
20 25 30
acg cgc gtg gag ctg cta acc ttc cag gag cgg tac tac aag atg aag 144
Thr Arg Val Glu Leu Leu Thr Phe Gln Glu Arg Tyr Tyr Lys Met Lys
35 40 45
gaa gag cgg gac agc tac aat gac gag ctg gtc aag gtg aag gac gac 192
Glu Glu Arg Asp Ser Tyr Asn Asp Glu Leu Val Lys Val Lys Asp Asp
50 55 60
aac tac aac tta gcc atg cgc tac gca cag ctc agt gag gag aag aac 240
Asn Tyr Asn Leu Ala Met Arg Tyr Ala Gln Leu Ser Glu Glu Lys Asn
65 70 75 80
atg gcg gtc atg agg agc cga gac ctc caa ctc gag atc gat cag cta 288
Met Ala Val Met Arg Ser Arg Asp Leu Gln Leu Glu Ile Asp Gln Leu
85 90 95
aag cac cgg ttg aat aag atg gag gag gaa tgt aag ctg gag aga aat 336
Lys His Arg Leu Asn Lys Met Glu Glu Glu Cys Lys Leu Glu Arg Asn
100 105 110
cag tct cta aaa ctg aag aat gac att gaa aat cgg ccc aag aag gag 384
Gln Ser Leu Lys Leu Lys Asn Asp Ile Glu Asn Arg Pro Lys Lys Glu
115 120 125
cag gtt ctg gaa ctg gag cgg gag aat gaa atg ctg aag acc aaa aac 432
Gln Val Leu Glu Leu Glu Arg Glu Asn Glu Met Leu Lys Thr Lys Asn
130 135 140
cag gag ctg cag tcc atc atc cag gcc ggg aag cgc agc ctg cca gac 480
Gln Glu Leu Gln Ser Ile Ile Gln Ala Gly Lys Arg Ser Leu Pro Asp
145 150 155 160
tca gac aag gcc atc ctg gac atc ttg gaa cac gac cgc aag gag gcc 528
Ser Asp Lys Ala Ile Leu Asp Ile Leu Glu His Asp Arg Lys Glu Ala
165 170 175

ctg gag gac agg cag gag ctg gtc aac agg atc tac aac ctg cag gag	576
Leu Glu Asp Arg Gln Glu Leu Val Asn Arg Ile Tyr Asn Leu Gln Glu	
180 185 190	
 gag gcc cgc cag gca gag gag ctg cga gac aag tac ctg gag gag aag	 624
Glu Ala Arg Gln Ala Glu Glu Leu Arg Asp Lys Tyr Leu Glu Glu Lys	
195 200 205	
 gag gac ctg gag ctc aag tgc tgc acc ctg gga aag gac tgt gaa atg	 672
Glu Asp Leu Glu Leu Lys Cys Ser Thr Leu Gly Lys Asp Cys Glu Met	
210 215 220	
 tac aag cac cgc atg aac acg gtc atg ctg cag ctg gag gag gtg gag	 720
Tyr Lys His Arg Met Asn Thr Val Met Leu Gln Leu Glu Glu Val Glu	
225 230 235 240	
 cgg gag cgg gac cag gga cag gct gtg gcc ttc cag gga cac tgc atc	 768
Arg Glu Arg Asp Gln Gly Gln Ala Val Ala Phe Gln Gly His Cys Ile	
245 250 255	
 aaa gct ctc aac aca gag cct gcc act agc aag ggt cgg acc atc ggc	 816
Lys Ala Leu Asn Thr Glu Pro Ala Thr Ser Lys Gly Arg Thr Ile Gly	
260 265 270	
 tct gtg atc gcg tta atg aag aag gcc ttc cac tcc cga gat gaa gct	 864
Ser Val Ile Ala Leu Met Lys Lys Ala Phe His Ser Arg Asp Glu Ala	
275 280 285	
 cag aca cag tac tgc cag tgc tta atc gaa aag gac aag tac agg aag	 912
Gln Thr Gln Tyr Ser Gln Cys Leu Ile Glu Lys Asp Lys Tyr Arg Lys	
290 295 300	
 cag atc cgc gag ctg gag gag aag aac gac gag atg agg atc gag	 957
Gln Ile Arg Glu Leu Glu Glu Lys Asn Asp Glu Met Arg Ile Glu	
305 310 315	

<210> 12
 <211> 319
 <212> PRT
 <213> Homo sapiens

<400> 12
 Lys Leu Gln Gln Gln Met Lys Ala Lys Asp Leu Gln Arg Cys Glu Leu
 1 5 10 15
 Leu Ala Arg Leu Arg Gln Leu Glu Asp Glu Lys Lys Gln Met Thr Leu
 20 25 30
 Thr Arg Val Glu Leu Leu Thr Phe Gln Glu Arg Tyr Tyr Lys Met Lys
 35 40 45
 Glu Glu Arg Asp Ser Tyr Asn Asp Glu Leu Val Lys Val Lys Asp Asp
 50 55 60
 Asn Tyr Asn Leu Ala Met Arg Tyr Ala Gln Leu Ser Glu Glu Lys Asn

65					70					75				80	
Met	Ala	Val	Met	Arg	Ser	Arg	Asp	Leu	Gln	Leu	Glu	Ile	Asp	Gln	Leu
				85					90					95	
Lys	His	Arg	Leu	Asn	Lys	Met	Glu	Glu	Glu	Cys	Lys	Leu	Glu	Arg	Asn
			100					105					110		
Gln	Ser	Leu	Lys	Leu	Lys	Asn	Asp	Ile	Glu	Asn	Arg	Pro	Lys	Lys	Glu
			115				120					125			
Gln	Val	Leu	Glu	Leu	Glu	Arg	Glu	Asn	Glu	Met	Leu	Lys	Thr	Lys	Asn
			130				135				140				
Gln	Glu	Leu	Gln	Ser	Ile	Ile	Gln	Ala	Gly	Lys	Arg	Ser	Leu	Pro	Asp
145					150					155					160
Ser	Asp	Lys	Ala	Ile	Leu	Asp	Ile	Leu	Glu	His	Asp	Arg	Lys	Glu	Ala
				165					170					175	
Leu	Glu	Asp	Arg	Gln	Glu	Leu	Val	Asn	Arg	Ile	Tyr	Asn	Leu	Gln	Glu
			180					185					190		
Glu	Ala	Arg	Gln	Ala	Glu	Glu	Leu	Arg	Asp	Lys	Tyr	Leu	Glu	Glu	Lys
			195				200					205			
Glu	Asp	Leu	Glu	Leu	Lys	Cys	Ser	Thr	Leu	Gly	Lys	Asp	Cys	Glu	Met
			210			215					220				
Tyr	Lys	His	Arg	Met	Asn	Thr	Val	Met	Leu	Gln	Leu	Glu	Glu	Val	Glu
225					230					235					240
Arg	Glu	Arg	Asp	Gln	Gly	Gln	Ala	Val	Ala	Phe	Gln	Gly	His	Cys	Ile
				245					250					255	
Lys	Ala	Leu	Asn	Thr	Glu	Pro	Ala	Thr	Ser	Lys	Gly	Arg	Thr	Ile	Gly
			260					265					270		
Ser	Val	Ile	Ala	Leu	Met	Lys	Lys	Ala	Phe	His	Ser	Arg	Asp	Glu	Ala
			275				280					285			
Gln	Thr	Gln	Tyr	Ser	Gln	Cys	Leu	Ile	Glu	Lys	Asp	Lys	Tyr	Arg	Lys
			290			295					300				
Gln	Ile	Arg	Glu	Leu	Glu	Glu	Lys	Asn	Asp	Glu	Met	Arg	Ile	Glu	
305					310					315					

<210> 13
 <211> 339
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(339)

<400> 13	
aag ttc tct ctg gaa aga ccc ttc cgg cct tcg gtc acc tct gtg ggg	48
Lys Phe Ser Leu Glu Arg Pro Phe Arg Pro Ser Val Thr Ser Val Gly	
1 5 10 15	
cac gtg cgg ggc cca ggg ccc tcg gtg cag cac acg acg ctg aat ggc	96
His Val Arg Gly Pro Gly Pro Ser Val Gln His Thr Thr Leu Asn Gly	
20 25 30	
gac agc ctc acc tcc cag ctc acc ctg ctg ggg ggc aac gcg cga ggg	144
Asp Ser Leu Thr Ser Gln Leu Thr Leu Leu Gly Gly Asn Ala Arg Gly	

35	40	45	
agc ttc gtg cac tcg gtc aag cct ggc tct ctg gcc gag aaa gcc ggc			192
Ser Phe Val His Ser Val Lys Pro Gly Ser Leu Ala Glu Lys Ala Gly			
50	55	60	
ctc cgt gag ggc cac cag ctg ctg ctg cta gaa ggc tgc atc cga ggc			240
Leu Arg Glu Gly His Gln Leu Leu Leu Leu Glu Gly Cys Ile Arg Gly			
65	70	75	80
gag agg cag agt gtc ccg ttg gac aca tgc acc aaa gag gaa gcc cac			288
Glu Arg Gln Ser Val Pro Leu Asp Thr Cys Thr Lys Glu Glu Ala His			
85	90	95	
tgg acc atc cag agg tgc agc ggc ccc gtc acg ctg cac tac aag gtc			336
Trp Thr Ile Gln Arg Cys Ser Gly Pro Val Thr Leu His Tyr Lys Val			
100	105	110	
aac			339
Asn			

<210> 14
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 14
Lys Phe Ser Leu Glu Arg Pro Phe Arg Pro Ser Val Thr Ser Val Gly
1 5 10 15
His Val Arg Gly Pro Gly Pro Ser Val Gln His Thr Thr Leu Asn Gly
20 25 30
Asp Ser Leu Thr Ser Gln Leu Thr Leu Leu Gly Gly Asn Ala Arg Gly
35 40 45
Ser Phe Val His Ser Val Lys Pro Gly Ser Leu Ala Glu Lys Ala Gly
50 55 60
Leu Arg Glu Gly His Gln Leu Leu Leu Leu Glu Gly Cys Ile Arg Gly
65 70 75 80
Glu Arg Gln Ser Val Pro Leu Asp Thr Cys Thr Lys Glu Glu Ala His
85 90 95
Trp Thr Ile Gln Arg Cys Ser Gly Pro Val Thr Leu His Tyr Lys Val
100 105 110
Asn

<210> 15
 <211> 417
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(417)

<221> misc_feature

<222> 416, 417

<223> n = A,T,C or G

<400> 15

atg	ggg	gaa	ctg	tgc	cgc	agg	gac	tcc	gca	ctc	acg	gca	ctg	gac	gag	48
Met	Gly	Glu	Leu	Cys	Arg	Arg	Asp	Ser	Ala	Leu	Thr	Ala	Leu	Asp	Glu	
1				5					10					15		

gag	aca	ctg	tgg	gag	atg	atg	gag	agc	cac	cgc	cac	agg	atc	gta	cgc	96
Glu	Thr	Leu	Trp	Glu	Met	Met	Glu	Ser	His	Arg	His	Arg	Ile	Val	Arg	
			20					25					30			

tgc	atc	tgc	ccc	agc	cgc	ctc	acc	ccc	tac	ctg	cgc	cag	gcc	aag	gtg	144
Cys	Ile	Cys	Pro	Ser	Arg	Leu	Thr	Pro	Tyr	Leu	Arg	Gln	Ala	Lys	Val	
		35					40					45				

ctg	tgc	cag	ctg	gac	gag	gag	gag	gtg	ctg	cac	agc	ccc	cgg	ctc	acc	192
Leu	Cys	Gln	Leu	Asp	Glu	Glu	Glu	Val	Leu	His	Ser	Pro	Arg	Leu	Thr	
	50					55					60					

aac	agc	gcc	atg	cgg	gcc	ggg	cac	ttg	ctg	gat	ttg	ctg	aag	act	cga	240
Asn	Ser	Ala	Met	Arg	Ala	Gly	His	Leu	Leu	Asp	Leu	Leu	Lys	Thr	Arg	
65					70					75					80	

ggg	aag	aac	ggg	gcc	atc	gcc	ttc	ctg	gag	agc	ctg	aag	ttc	cac	aac	288
Gly	Lys	Asn	Gly	Ala	Ile	Ala	Phe	Leu	Glu	Ser	Leu	Lys	Phe	His	Asn	
				85					90					95		

cct	gac	gtc	tac	acc	ctg	gtc	acc	ggg	ctg	cag	cct	gat	gtt	gac	ttc	336
Pro	Asp	Val	Tyr	Thr	Leu	Val	Thr	Gly	Leu	Gln	Pro	Asp	Val	Asp	Phe	
			100					105						110		

agt	aac	ttt	agc	ggt	gag	agc	tcc	gac	ttt	gac	ggt	ttg	gca	ggc	act	384
Ser	Asn	Phe	Ser	Gly	Glu	Ser	Ser	Asp	Phe	Asp	Gly	Leu	Ala	Gly	Thr	
		115					120					125				

tct	agg	aac	ctc	agg	ctc	ctg	gta	acc	cca	gnn						417
Ser	Arg	Asn	Leu	Arg	Leu	Leu	Val	Thr	Pro	Xaa						
		130				135										

<210> 16

<211> 139

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> 139

<223> Xaa = Any Amino Acid

<400> 16

Met	Gly	Glu	Leu	Cys	Arg	Arg	Asp	Ser	Ala	Leu	Thr	Ala	Leu	Asp	Glu
1				5					10					15	
Glu	Thr	Leu	Trp	Glu	Met	Met	Glu	Ser	His	Arg	His	Arg	Ile	Val	Arg
		20						25					30		
Cys	Ile	Cys	Pro	Ser	Arg	Leu	Thr	Pro	Tyr	Leu	Arg	Gln	Ala	Lys	Val
	35						40					45			
Leu	Cys	Gln	Leu	Asp	Glu	Glu	Val	Leu	His	Ser	Pro	Arg	Leu	Thr	
	50					55				60					
Asn	Ser	Ala	Met	Arg	Ala	Gly	His	Leu	Leu	Asp	Leu	Leu	Lys	Thr	Arg
65					70					75					80
Gly	Lys	Asn	Gly	Ala	Ile	Ala	Phe	Leu	Glu	Ser	Leu	Lys	Phe	His	Asn
			85						90					95	
Pro	Asp	Val	Tyr	Thr	Leu	Val	Thr	Gly	Leu	Gln	Pro	Asp	Val	Asp	Phe
		100						105					110		
Ser	Asn	Phe	Ser	Gly	Glu	Ser	Ser	Asp	Phe	Asp	Gly	Leu	Ala	Gly	Thr
	115						120					125			
Ser	Arg	Asn	Leu	Arg	Leu	Leu	Val	Thr	Pro	Xaa					
	130					135									

<210> 17

<211> 276

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(276)

<400> 17

gag	gag	aca	ctg	tgg	gag	atg	atg	gag	agc	cac	cgc	cac	agg	atc	gta	48
Glu	Glu	Thr	Leu	Trp	Glu	Met	Met	Glu	Ser	His	Arg	His	Arg	Ile	Val	
1				5					10					15		
cgc	tgc	atc	tgc	ccc	agc	cgc	ctc	acc	ccc	tac	ctg	cgc	cag	gcc	aag	96
Arg	Cys	Ile	Cys	Pro	Ser	Arg	Leu	Thr	Pro	Tyr	Leu	Arg	Gln	Ala	Lys	
			20					25					30			
gtg	ctg	tgc	cag	ctg	gac	gag	gag	gag	gtg	ctg	cac	agc	ccc	cgg	ctc	144
Val	Leu	Cys	Gln	Leu	Asp	Glu	Glu	Glu	Val	Leu	His	Ser	Pro	Arg	Leu	
		35					40					45				
acc	aac	agc	gcc	atg	cgg	gcc	ggg	cac	ttg	ctg	gat	ttg	ctg	aag	act	192
Thr	Asn	Ser	Ala	Met	Arg	Ala	Gly	His	Leu	Leu	Asp	Leu	Leu	Lys	Thr	
	50					55					60					
cga	ggg	aag	aac	ggg	gcc	atc	gcc	ttc	ctg	gag	agc	ctg	aag	ttc	cac	240
Arg	Gly	Lys	Asn	Gly	Ala	Ile	Ala	Phe	Leu	Glu	Ser	Leu	Lys	Phe	His	
	65				70					75					80	

aac cct gac gtc tac acc ctg gtc acc ggg ctg cag
Asn Pro Asp Val Tyr Thr Leu Val Thr Gly Leu Gln
85 90

276

<210> 18
<211> 92
<212> PRT
<213> Homo sapiens

<400> 18
Glu Glu Thr Leu Trp Glu Met Met Glu Ser His Arg His Arg Ile Val
1 5 10 15
Arg Cys Ile Cys Pro Ser Arg Leu Thr Pro Tyr Leu Arg Gln Ala Lys
20 25 30
Val Leu Cys Gln Leu Asp Glu Glu Val Leu His Ser Pro Arg Leu
35 40 45
Thr Asn Ser Ala Met Arg Ala Gly His Leu Leu Asp Leu Leu Lys Thr
50 55 60
Arg Gly Lys Asn Gly Ala Ile Ala Phe Leu Glu Ser Leu Lys Phe His
65 70 75 80
Asn Pro Asp Val Tyr Thr Leu Val Thr Gly Leu Gln
85 90

<210> 19
<211> 2176
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (147)...(1247)

<400> 19
atcatcagga agtgcacagg cgtccggcgt gctcctccct ccctgcagcc ccgggcagca 60
tctcccagag gctccgcggc ccaggctcct ggtgtgtctg cagtgcaggt ggctcctgga 120
agaccctcag cctgcctgct gaggcc atg tcg gac tac gag aac gat gac gag 173
Met Ser Asp Tyr Glu Asn Asp Asp Glu
1 5

tgc tgg aac gtc ctg gag ggc ttc cgg gtg acg ctc acc tcg gtc atc 221
Cys Trp Asn Val Leu Glu Gly Phe Arg Val Thr Leu Thr Ser Val Ile
10 15 20 25

gac ccc tca cgc atc aca cct tac ctg cgg cag tgc aag gtc ctg aac 269
Asp Pro Ser Arg Ile Thr Pro Tyr Leu Arg Gln Cys Lys Val Leu Asn
30 35 40

cct gat gat gag gag cag gtg ctc agc gac ccc aac ctg gtc atc cgc 317
Pro Asp Asp Glu Glu Gln Val Leu Ser Asp Pro Asn Leu Val Ile Arg
45 50 55

aaa cgg aaa gtg ggt gtg ctc ctg gac atc ctg cag cgg acc ggc cac	365
Lys Arg Lys Val Gly Val Leu Leu Asp Ile Leu Gln Arg Thr Gly His	
60 65 70	
aag ggc tac gtg gcc ttc ctc gag agc ctg gag ctc tac tac ccg cag	413
Lys Gly Tyr Val Ala Phe Leu Glu Ser Leu Glu Leu Tyr Tyr Pro Gln	
75 80 85	
ctg tac aag aag gtc aca ggc aag gag ccg gcc cgc gtc ttc tcc atg	461
Leu Tyr Lys Lys Val Thr Gly Lys Glu Pro Ala Arg Val Phe Ser Met	
90 95 100 105	
atc atc gac gcg tcc ggg gag tca ggc ctg act cag ctg ctg atg act	509
Ile Ile Asp Ala Ser Gly Glu Ser Gly Leu Thr Gln Leu Leu Met Thr	
110 115 120	
gag gtc atg aag ctg cag aag aag gtg cag gac ctg acc gcg ctg ctg	557
Glu Val Met Lys Leu Gln Lys Lys Val Gln Asp Leu Thr Ala Leu Leu	
125 130 135	
agc tcc aaa gat gac ttc atc aag gag ctg cgg gtg aag gac agc ctg	605
Ser Ser Lys Asp Asp Phe Ile Lys Glu Leu Arg Val Lys Asp Ser Leu	
140 145 150	
ctg cgc aag cac cag gag cgt gtg cag agg ctc aag gag gag tgc gag	653
Leu Arg Lys His Gln Glu Arg Val Gln Arg Leu Lys Glu Glu Cys Glu	
155 160 165	
gcc ggc agc cgc gag ctc aag cgc tgc aag gag gag aac tac gac ctg	701
Ala Gly Ser Arg Glu Leu Lys Arg Cys Lys Glu Glu Asn Tyr Asp Leu	
170 175 180 185	
gcc atg cgc ctg gcg cac cag agt gag gag aag ggc gcc gcg ctc atg	749
Ala Met Arg Leu Ala His Gln Ser Glu Glu Lys Gly Ala Ala Leu Met	
190 195 200	
cgg aac cgt gac ctg cag ctg gag att gac cag ctc aag cac agc ctc	797
Arg Asn Arg Asp Leu Gln Leu Glu Ile Asp Gln Leu Lys His Ser Leu	
205 210 215	
atg aag gcc gag gac gac tgc aag gtg gag cgc aag cac acg ctg aag	845
Met Lys Ala Glu Asp Asp Cys Lys Val Glu Arg Lys His Thr Leu Lys	
220 225 230	
ctc agg cac gcc atg gag cag cgg ccc agc cag gag ctg ctg tgg gag	893
Leu Arg His Ala Met Glu Gln Arg Pro Ser Gln Glu Leu Leu Trp Glu	
235 240 245	
ctg cag cag gag aag gcc ctg ctc cag gcc cgg gtg cag gag ctg gag	941
Leu Gln Gln Glu Lys Ala Leu Leu Gln Ala Arg Val Gln Glu Leu Glu	
250 255 260 265	
gcc tcc gtc cag gag ggg aag ctg gac agg agc agc ccc tac atc cag	989

Ala Ser Val Gln Glu Gly Lys Leu Asp Arg Ser Ser Pro Tyr Ile Gln
270 275 280

gta ctg gag gag gac tgg cgg cag gcg ctg cgg gac cac cag gag cag 1037
Val Leu Glu Glu Asp Trp Arg Gln Ala Leu Arg Asp His Gln Glu Gln
285 290 295

gcc aac acc atc ttc tcc ctg cgc aag gac ctc cgc cag ggc gag gcc 1085
Ala Asn Thr Ile Phe Ser Leu Arg Lys Asp Leu Arg Gln Gly Glu Ala
300 305 310

cga cgc ctc cgg tgc atg gag gag aag gag atg ttc gag ctg cag tgc 1133
Arg Arg Leu Arg Cys Met Glu Glu Lys Glu Met Phe Glu Leu Gln Cys
315 320 325

ctg gca cta cgt aag gac tcc aag atg tac aag gac cgc atc gag gcc 1181
Leu Ala Leu Arg Lys Asp Ser Lys Met Tyr Lys Asp Arg Ile Glu Ala
330 335 340 345

atc ctg ctg cag atg gag gag gtc gcc att gag cgg gac cag agc aca 1229
Ile Leu Leu Gln Met Glu Glu Val Ala Ile Glu Arg Asp Gln Ser Thr
350 355 360

caa atg gag ggg ctg tga ccagcctccg cgcccagcgg cttgacgtcc 1277
Gln Met Glu Gly Leu *
365

tccggagcct ctgcttggag ttgggaggcc gggccgaggg cccagggcaa gcttggggcc 1337
ctcactgagg gtcggccttg tgctgtcccg tcaggccata gccacgcggg aggagctgca 1397
cgcacagcac gcccggggccc tgcaggagaa ggacgcgctg cgcaagcagg tgcgggagct 1457
gggcgagaag gcgatgagc tgcagctgca ggtgttccag tgtgaggcgc agctactggc 1517
cgtggagggc aggtcaggc ggcagcagct ggagacgctc gtcctgagct ccgacctgga 1577
agatgggtca cccaggaggt cccaggagct ctcactcccc caggacctgg aggacacca 1637
gctctcagac aaaggctgcc ttgccggcgg ggggagcccg aaacagccct ttgcagctct 1697
gcaccaggag caggttttgc ggaacccccca tgacgcaggc ctgagcagcg gggagccgcc 1757
cgagaaggag cggcggcgcc tcaaagagag ttttgagaac taccgcagga agcgcgccct 1817
caggaagatg cagaaaggat ggcggcaggg ggaggaggac cgggagaaca ccacgggcag 1877
cgacaacacc gacactgagg gtcctagcc gcagcagact tccccgagcc gtcgctgact 1937
tggcctgga caggaatct ggtgccctga aaggcccagc cggactgccg ggcattgggg 1997
ccgtttgtta agcggcactc attttgcgga ggccatgcgg gtgctacca ccccatgca 2057
cacgccatct gtgtaacttc aggatctgtt ctgtttcacc atgtaacaca caatacatgc 2117
atgcattgta ttagtgtag aaaacacagc tgcgtaaata aacagcacgg gtgaccgc 2176

<210> 20
<211> 366
<212> PRT
<213> Homo sapiens

<400> 20
Met Ser Asp Tyr Glu Asn Asp Asp Glu Cys Trp Asn Val Leu Glu Gly
1 5 10 15
Phe Arg Val Thr Leu Thr Ser Val Ile Asp Pro Ser Arg Ile Thr Pro
20 25 30

Tyr	Leu	Arg	Gln	Cys	Lys	Val	Leu	Asn	Pro	Asp	Asp	Glu	Glu	Gln	Val
	35						40					45			
Leu	Ser	Asp	Pro	Asn	Leu	Val	Ile	Arg	Lys	Arg	Lys	Val	Gly	Val	Leu
	50					55					60				
Leu	Asp	Ile	Leu	Gln	Arg	Thr	Gly	His	Lys	Gly	Tyr	Val	Ala	Phe	Leu
65					70					75					80
Glu	Ser	Leu	Glu	Leu	Tyr	Tyr	Pro	Gln	Leu	Tyr	Lys	Lys	Val	Thr	Gly
			85						90					95	
Lys	Glu	Pro	Ala	Arg	Val	Phe	Ser	Met	Ile	Ile	Asp	Ala	Ser	Gly	Glu
		100						105					110		
Ser	Gly	Leu	Thr	Gln	Leu	Leu	Met	Thr	Glu	Val	Met	Lys	Leu	Gln	Lys
	115						120					125			
Lys	Val	Gln	Asp	Leu	Thr	Ala	Leu	Leu	Ser	Ser	Lys	Asp	Asp	Phe	Ile
	130					135					140				
Lys	Glu	Leu	Arg	Val	Lys	Asp	Ser	Leu	Leu	Arg	Lys	His	Gln	Glu	Arg
145					150					155					160
Val	Gln	Arg	Leu	Lys	Glu	Glu	Cys	Glu	Ala	Gly	Ser	Arg	Glu	Leu	Lys
			165						170					175	
Arg	Cys	Lys	Glu	Asn	Tyr	Asp	Leu	Ala	Met	Arg	Leu	Ala	His	Gln	
		180					185					190			
Ser	Glu	Glu	Lys	Gly	Ala	Ala	Leu	Met	Arg	Asn	Arg	Asp	Leu	Gln	Leu
	195						200					205			
Glu	Ile	Asp	Gln	Leu	Lys	His	Ser	Leu	Met	Lys	Ala	Glu	Asp	Asp	Cys
	210					215					220				
Lys	Val	Glu	Arg	Lys	His	Thr	Leu	Lys	Leu	Arg	His	Ala	Met	Glu	Gln
225					230					235					240
Arg	Pro	Ser	Gln	Glu	Leu	Leu	Trp	Glu	Leu	Gln	Gln	Glu	Lys	Ala	Leu
			245						250					255	
Leu	Gln	Ala	Arg	Val	Gln	Glu	Leu	Glu	Ala	Ser	Val	Gln	Glu	Gly	Lys
		260						265					270		
Leu	Asp	Arg	Ser	Ser	Pro	Tyr	Ile	Gln	Val	Leu	Glu	Glu	Asp	Trp	Arg
	275						280					285			
Gln	Ala	Leu	Arg	Asp	His	Gln	Glu	Gln	Ala	Asn	Thr	Ile	Phe	Ser	Leu
	290					295					300				
Arg	Lys	Asp	Leu	Arg	Gln	Gly	Glu	Ala	Arg	Arg	Leu	Arg	Cys	Met	Glu
305					310					315					320
Glu	Lys	Glu	Met	Phe	Glu	Leu	Gln	Cys	Leu	Ala	Leu	Arg	Lys	Asp	Ser
			325						330					335	
Lys	Met	Tyr	Lys	Asp	Arg	Ile	Glu	Ala	Ile	Leu	Leu	Gln	Met	Glu	Glu
		340						345					350		
Val	Ala	Ile	Glu	Arg	Asp	Gln	Ser	Thr	Gln	Met	Glu	Gly	Leu		
	355						360					365			

<210> 21
 <211> 281
 <212> DNA
 <213> Homo sapiens

<400> 21
 gagaggctcc gcggcccagg ctcttggtgt gtctgcagtg caggtggctc ctggaagacc 60
 ctcagcctgc ctgctgaggc catgtttgac tacgagaacg atgacgagtg ctggagcgtc 120
 ctggaggggt tccgggtgac gctcacctcg gtcacgcacc cctcacgcat cacaccttac 180

```
ctgcggcagt gcaaggctct gaaccccgat gatgaggagc aggtgctcag cgaccccaac 240
ctgggtcatcc gcaaacggaa agtgggtgtg ctcttgga t 281
```

<210> 22

<211> 734

<212> DNA

<213> Gallus gallus

<400> 22

```
gggacagcct gctccgcaag caccaagagc ggggtgcagaa gatgagggag gagagggaca 60
gtctaagcaa ggagctgcgg aagtgcagg atgagaacta caacctggca atgagctatg 120
ccagacagag cgaggagaag agcagtgcc tcatgaagaa cagggacctg ctcttagaga 180
ttgatagctt gaagcatagc ctcatgaagg ctgaggacga ctgcaaacta gagcgttaagc 240
actcgatgaa actgaagcat gccatagaac aacgtccgag ccatgaagtg atgtgggaga 300
tccagcagga gaaggagctg cttttggcca agaatacagga gctggagaac actcttcagg 360
ttgccaggga acagaatttg gagacgagtc tctcccatga gactgtgcag aatgactgca 420
gccagggtgct ggagcgccag gacctgctga acacctgta ccaccttcgc aaggagctgc 480
gccaagccga ggtgcttcga gacaagttcg aggagtgagc ctgagccac gaggagctgt 540
ccgagaagga gcggaggagg atgaaggact gctttgagcg ttaccgcagg aagcgcgccc 600
tgcgcagagc gccgcggggc ccgcccgcgc gagggcgact gggagccgag cacgggcagc 660
gacaacacgg acaccgaggg cagctagggg ccgcccagagc tttcgagttt gcagctggat 720
ccgtcaataa acag 734
```

<210> 23

<211> 630

<212> DNA

<213> Gallus gallus

<400> 23

```
tgaacaccct gtaccacctt cgcaaggagc tgcgccaaagc cgagggtgctc cgagacaagt 60
atgcagagga aaaagaaata cttgaactac agtgcacatc tctgaggaag gactcccaga 120
tgtataaaaa acggatggaa gctgtcttag agcagatgga ggaagtggct tcggaaagag 180
accaggcact gctgaccaga gaacagttct acccacagta ctccaagaac cttgttgaga 240
gggacactta tcggaagcag attcgggagc tgggggagcg atgcgatgag ctgcagctgc 300
agctcttcca aaaggagggg cagctactgg ctactgaagc caagctgaaa agactgcaac 360
tggagctgcc tgcactgact tctgacctgg atgacactcc tccagagatc ccaggcttta 420
ctctcatggt catctagacg aagatcgcac ctgactaaaa aagacgctgt taaggaaaac 480
cagcaatcag catgcaagaa acatctgacg cagatcacca cttcgaggat gcactaacca 540
caagacttcg agaagacgga gagataagga tgcttgagcg tacgagtcgg ccgatccgcg 600
ccccccctcc gcgctccttc cgtggctcgt 630
```

<210> 24

<211> 331

<212> DNA

<213> Homo sapiens

<400> 24

```
cacgagggaa atgtacaagc accgcatgaa cacggtcatg ctgcacctgg aggaggtgga 60
gcgggagcgg gaccaggcct tccactcccg agatgaagct cagacacagt actcgagtg 120
cttaatcgaa aaggacaagt acaggaagca gatccgcgag ctggaggaga agaacgacga 180
gatgaggatc gagatggtgc ggcgggaggg ctgcatcgct aacctggaga gcaagctgcg 240
gcgcctctcc aaggacagca acaacctgga ccagagtctg cccaggaacc tgccagtaac 300
catcatctct caggactttg gggatgccag c 331
```

<210> 25
<211> 478
<212> DNA
<213> Homo sapiens

<400> 25
tttttttttt tttttctctc ctgcctcctc tggccttcgg actcctgccc gcgcccggcg 60
cagccccctc ccggccctgc agccccctggg cgggcggcgc ccctcggagg acggctccgg 120
gcccgggggg acggagggcc tggtcgcctg gaggaagccg gaggcctgcg tggaggaggc 180
gccccgcgca gctggctggc ggagcatgag cgccccagat cccaagcact gcaagtccag 240
atgcaacggg agcctggctc aagggacgac aagatccagc cggaagtgt agaagtcaca 300
ccccaatggc gggatagcag cccctgtgtg tgagcacccc tccatgccag gaggagggcc 360
agagatggat gactacatgg agaccctgaa ggatgaagag gacccttgt gggacaatgt 420
ggagtgtaac cggcacatgc tcaaccgcta tatcaaccct gccaaagtca cgccctac 478

<210> 26
<211> 396
<212> DNA
<213> Homo sapiens

<400> 26
gcagccccct cccggccctg cagccccctgg cgtgcggcgc catcggayga cggctccggg 60
cccgggggga cggagggcct ggtcgcctgg aggaagccgg acgctgcgtg gaggaggcgc 120
ccccggtctg gtctggcgga cgatgagcgc ccagatccc aagcactgca agtccagatg 180
caacggggagc ctggctcaag ggacgacaag atccagccgg aaagtgtaga agtcacaccc 240
caatggcggg atagcagccc ctgtgtgtga tcaccctcc atgccaggag gagggccaga 300
gatggatgac tacatggaga cgctgaatga tgaagaggac gccttgtggg agaattgtga 360
gtgtaaccgg cacatgctca gccgctatat caaccc 396

<210> 27
<211> 162
<212> DNA
<213> Homo sapiens

<400> 27
aaaaggagga gggccagaga tggatgacta catggagacg ctgaaggatg aagaggacgc 60
cttgtgggtg aatgtggagt gtaaccggca catgctcagc cgggtctcac gaattccgct 120
gagttctcac gaattccgct gaggtctcac gaattccgct ga 162

<210> 28
<211> 418
<212> DNA
<213> Homo sapiens

<400> 28
cacgacgacg gacgccagcc ctagctcctg cggatctctg cccatcacca actccttcac 60
caagatgcag ccccccgga gccgcagcag catcatgtca atcaccgccg agccccggg 120
aaacgactcc atcgtcagac gctacaagga ggacgcgccc catcgcagca cagtccaaga 180
agacaatgac agcggcgggt ttgacgcctt agatctggat gatgacagtc acgaacgcta 240
ctccttcgga cctcctcca tccactcctc ctccctctcc caccaatccg agggcctgga 300
tgcctacgac ctggagcagg tcaacctcat gtccaggaag ttctctctgg aaagaccctt 360
ccggccttcg gtcacctctg tggggcacgt tcggggccca aggccttcgg tgcagcac 418

<210> 29
<211> 610
<212> DNA
<213> Homo sapiens

<400> 29
tcatccccta cagcctggta cgcgctttct actgcgagcg ccgccggccc gtgctcttca 60
caccaccgt gctggccaag acgctggtgc agaggctgct caactcggga ggtgccatgg 120
agttcaccat ctgcaagtca gatatcgtca caagagatga gttcctcaga aggcagaaga 180
cggagaccat catctactcc cgagagaaga accccaacgc gttcgaatgc atcgcccctg 240
ccaacatcga agctgtggcc gccaagaaca agcactgcct gctggaggct gggatcggct 300
gcacaagaga cttgatcaag tccaacatct accccatcgt gctcttcac cgggtgtgtg 360
agaagaacat caagaggttc agaaagctgc tgccccgacc tgagacggag gaggagtcc 420
tgcgcggtgtg ccggtgaag gagaaggagc tggaggccct gccgtgcctg tacgccacgg 480
tggaacctga catgtggggc agcgtagagg agctgtcccg cgttgtaag gacaagatcg 540
gcgaggagca gcgcaagacc atctgggtgg acgaggacca gctgtgaggc gggcgccctg 600
ggcagagaga 610

<210> 30
<211> 556
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 470
<223> n = A,T,C or G

<400> 30
tcatccccta cagcctggta cgcgctttct actgcgagcg ccgccggccc gtgctcttca 60
caccaccgt gctggccaag acgctggtgc agaggctgct caactcggga ggtgccatgg 120
agttcaccat ctgcaagtca gatatcgtca caagagatga gttcctcaga aggcagaaga 180
cggagaccat catctactcc cgagagaaga accccaacgc gttcgaatgc atcgcccctg 240
ccaacatcga agctgtggcc gccaagaaca agcactgcct gctggaggct gggatcggct 300
gcacaagaga cttgatcaag tccaacatct accccatcgt gctcttcac cgggtgtgtg 360
agaagaacat caagaggttc agaaagctgc tgccccgacc tgagacggag gaggagtcc 420
tgcgcggtgtg ccggtgaag gagaaggagc tggaggccct gccgttgccn tggtagccca 480
cgggtggaacc tgacatgtgg ggcagcgtag aggagctgct ccgcgtgtca ggacagacgg 540
cgagagcagc gcaaga 556

<210> 31
<211> 390
<212> DNA
<213> Homo sapiens

<400> 31
gtccttcag ttcgtcagca ggtccgagaa caagtataag cggatgaaca gcaacgagcg 60
ggtccgatca tctcggggag tccgctagga gcctggcccc gtcctcgtg gacgccacca 120
agctcttgac tgagaagcag gaagagctgg accctgagag cgagctgggc aagaacctca 180
gcctcatccc ctacagcctg gtacgcgcct tctactgcga gcgcgcgcgg cctgtgtctt 240
tcacaccac cgtgtgtggc aagacgctgg tgagaggct gctcaactcg ggaggtgcca 300
tggagttcac catctgcaag tcagatatcg tcacaagaga tgagttcctc agaaggcaga 360

agacggagac catcatctac tcccagagaga

390

<210> 32

<211> 620

<212> DNA

<213> Homo sapiens

<400> 32

```
agagacttga tcaagtccaa catctacccc atcgtgctct tcatccgggt gtgtgagaag 60
aacatcaaga ggttcagaaa gctgctgccc cggcctgaga cggaggagga gttcctgcgc 120
gtgtgccggc tgaaggagaa ggagctggag gccctgccgt gcctgtacgc cacggtggaa 180
cctgacatgt ggggcagcgt agaggagctg ctccgcgttg tcaaggacaa gatcggcgag 240
gagcagcgca agaccatctg ggtggacgag gaccagctgt gaggcgggcg ccctgggcag 300
agagactctg tggcgcgggg catcctatga ggcaggcacc ctgggcagag agatgtagtg 360
ggtgcggggg gatcctgtgg cccacagagc tgccccagca gacgctccgc cccacccggt 420
gatggagccc cggggggaca gtcgtgcctg gggaggagca gggtagagcc cattccccca 480
gccctggctg acctggccta gcagttttgg ccctgctggc cttagcaggg agacagggga 540
gcaaagaacg ccaagccggg aggcccaagc cagccggggt ctcgaggggg ggcccgggtcc 600
ccattttgcc ctttatgagc                                     620
```

<210> 33

<211> 283

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 42, 85, 109, 111, 139, 222, 244, 263

<223> n = A,T,C or G

<400> 33

```
aagagacttg atcaagtcca acatctaccc catcgtgctc tntcatccgg gtgtgtgaga 60
agaacatcaa gaggttcaga aagcngctgc cccggcctga gacggaggng nagttcctgc 120
gcgtgtgccg gctgaaggng aaggagctgg aggccctgcc gtgcctgtac gcgacggtgg 180
aacctgacat gtggggcagc gtagaggagc tgctccgcgt tntataagga caagatcggg 240
gagnagcagc gcaagaccat ctnggtagac gaggaccagc ttt                                     283
```

<210> 34

<211> 207

<212> DNA

<213> Homo sapiens

<400> 34

```
gtgtactgcc ttctgaggaa ctcatctctg tgacgatatc tgacttgagc atggtgaact 60
ccatggcacc tcccaggttg agcagcctct gcaccagcgt cttggccagc acggtggggtg 120
tgaagagcac gggccggcgg cgctcgagc agaaggcgcg taccaggctg taggggatga 180
ggctgaggtt cttgcccagc tcgctct                                     207
```

<210> 35

<211> 192

<212> DNA

<213> Homo sapiens

<400> 35
gacttgatca agtccaacat ctaccccatc gtgctcttca tccgggtgtg tgagaagaac 60
atcaagaggt tcagaaagct gctgccccgg cctgagactg gaggaggagt tcctgcgcgt 120
gtgccggctg aaggagaagg agctggaggc cctgcgatgc ctgtacgcca cgggtggaacc 180
tgacatgtgg gg 192

<210> 36
<211> 605
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 213
<223> n = A,T,C or G

<400> 36
gaaataataa tacattttta tgcaagagaa atcatagcct ggtacacacc ctttccccga 60
tctgtcctgc ctggggatgt gtttatgggt agtgtgtccc caggactggt agtcacctgg 120
ctgtccgggt cccgcacctg ctggcggcag catgcctgtc ccagcatta cattcaactg 180
ctgctcttgc tctcgagagg ccggctggcc tcnggccttc cggcttggcg ttctttgtct 240
ccctgtctcc ctgctaaggc cagcagggcc aaactgctag gccaggtcag ccagggtcgg 300
gggaatgggc tgtacctgc tcttccccag gcacgactgt cccccgggg ctccatcacc 360
gggtggggcg gagcgtctgc tggggcagct ctgtgggcca caggatcccc ccgcaccac 420
tgcatctctc tgcccatggt gcctgcctca taggatgcc cgcgccacag agtctatatg 480
tccagggcgc ccgcctcaca gctggctctc gtccaccag atggtcttgc gctgctcctc 540
gccgatcttg tccttgacat cgcggagcag ctcttttacg ctgccccaca tgtcagggtgc 600
ccccg 605

<210> 37
<211> 1141
<212> DNA
<213> Homo sapiens

<400> 37
tcatgcccag ctccgtccca cccagcagcc cgcagagaaa ggaggcagct ggcaccacac 60
tgggcttttg agacactgcg gggactgtgg accccacctt gctgcacgga gctcctgcaa 120
aagcaaacct gagaaccttg ggtcctccca gcgccagcc atgggggaac tgtgccgcag 180
ggactccgca ctacggcac tggacgagga gacactgtgg gagatgatgg agagccaccg 240
ccacaggatc gtacgttgca tctgccccag acgacattaa cccctatact gtgacgcaca 300
gcgccagagg ctggctgctg accatggatg gaccgaggag ggaggttgct gcaccagcgc 360
ccacgagaca tcaacaacag acgcacactg cggggccggg cacatagcgt ggctctgcgc 420
tagaaagaca tcagaggaga aagaagcggg ggccactcg cactcacctg gagtagacgc 480
catgcacagt accaccaaac ccatgagcgc tactacaacc catgggtcac cagggcataga 540
cagcctggat gcatagacat aacaagtaac ttctactagc caggctctca tgcgaagacc 600
atcccaagcc tgacccgaca tgccctggac atggggccca ctacgcgcag accatgcagc 660
gagagacgca tgacaccagg caacaacgcg ggccacgaac gcgagcgttg cctgcatcga 720
cgggcacggt tggccacaga cacggaattg cagcggagcc acacgtggca gcccctgagg 780
cccagcgaca cccggtgcac cgaagggggc atggcaacca cgacctggca ggcttgacac 840
accaagcgcc ataccacgcg cgtgaaaggg tacagaggca ccaactaccc agtgcaagcg 900
cagttcttgc aaggcgatgc caagggaacg gcacgacatg acgacaccgc agtactctgt 960
gaggaaacca tcttagcaag atgacagcct tgacaggaaa caacgacacg aagtgcctgt 1020
ctcgcaacgc atgacagaag acctgtcgca tataaagtaa atgtgatact aatagaaagc 1080

aagaagggtg acactgaaag acacacatat gagtataact cgagtatgca acgtgaacat 1140
g 1141